

INVITED LECTURE H2

Continuing innovation in the post-proteomic world: the case for accurate mass tandem mass spectrometry in top down, bottom up and everything in between

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Now that proteomics using mass spectrometry has become a reality for many hundreds of laboratories world wide, how will this field continue to mature? One answer lies in the steady improvement in mass spectrometers, such as the low part-per-million mass accuracy of measuring intact peptides/proteins *and* their fragment ions. Another new development in computational proteomics is to house known information such as DNA polymorphisms, mRNA splicing events, and of course post-translational modifications for primary database searching using MS/MS acquired with accurate mass. Such advances will be highlighted, along with progress in Top Down Proteomics generally.